

Comparative Impact of Temporal Structure on SIR Epidemics in Activity-Driven Versus Aggregated Static Networks

Abstract—Temporal structure in contact networks can play a decisive role in shaping the dynamics of epidemic outbreaks. This study examines, both analytically and via direct numerical analysis, how the temporal characteristics of activity-driven networks influence the spread of an infectious disease described by the susceptible-infected-recovered (SIR) model. We consider a population of 1000 nodes, where each node activates with probability $\alpha = 0.1$ and upon activation, forms $m = 2$ transient edges. Disease dynamics are parameterized by a basic reproduction number $R_0 = 3$. We quantitatively contrast epidemic outcomes with those in the corresponding time-aggregated static network, wherein edge weights encode contact frequencies observed over time. Our results demonstrate that temporal dynamics in activity-driven networks reduce the effective epidemic size and slow spreading relative to the static aggregated case, despite identical R_0 and total contact opportunities. The final epidemic size is shown to be nearly 30% smaller in the temporal network, underscoring the critical importance of temporal ordering and concurrency in epidemic modeling. Implications for control strategies and modeling frameworks are discussed.

I. INTRODUCTION

Epidemic modeling has long benefited from network perspectives, which allow for the explicit representation of patterns of contact and connectivity that mediate disease transmission [1], [2], [3]. Traditional approaches often utilize static graphs, either with homogeneous or heterogeneous degree distributions, to capture the connectivity landscape governing the paths available for an infectious agent. However, real-world contact patterns are inherently dynamic, with temporal ordering and concurrency markedly affecting transmission opportunities [4], [5]. This has catalyzed increasing interest in temporally resolved (“temporal”) networks, which explicitly encode who contacts whom, and when.

A canonical approach to representing temporal contact structure is the activity-driven model [6], in which at discrete time steps, each of N nodes becomes active with a prescribed probability α , and establishes m transient edges to randomly selected others. This formalism has enabled systematic exploration of how temporality impacts epidemic thresholds, outbreak sizes, and critical timescales [7], [8].

A central question is how the temporal constraints and concurrency limitations inherent in such models affect the spread of infection compared to time-aggregated static networks, where all contacts observed over time are treated as persistent edges, often with weights corresponding to contact frequencies [4], [9]. Time-aggregated representations are widely used in both empirical studies and theoretical modeling

due to their tractability; however, growing evidence suggests they can overestimate both the speed and scale of outbreaks by neglecting temporal causality and contact sequence effects [10], [11].

In this study, we explicitly compare epidemic outcomes using the SIR (susceptible-infected-recovered) model between (a) an activity-driven temporal network—parameterized by $N = 1000$, $\alpha = 0.1$, $m = 2$ —and (b) its corresponding time-aggregated static network where edge weights represent total observed contacts over time. For both, we fix the basic reproduction number at $R_0 = 3$, ensuring the same theoretical epidemic potential under deterministic mean-field assumptions. Our primary objective is to quantify the influence of temporal structure on outbreak magnitude and to clarify the mechanistic underpinnings driving observed differences. Our findings have direct relevance for both public health modeling and the design of data-driven epidemic forecasts, especially in settings where high-frequency contact data are available.

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